

Result No.	Score	Query #		DB	ID	Description
		Match	Length			
1	2911	88.5	578	11	Q912D3	Q912d3 mus musculus
2	2885.5	87.7	609	11	Q923T5	Q923t5 mus musculus
3	2809.5	85.4	561	11	Q91V88	Q91v88 mus musculus
4	2784	84.6	592	11	Q91X15	Q91x15 mus musculus
5	1096	33.3	554	4	Q9NY67	Q9ny67 homo sapien
6	1092.5	33.2	553	4	Q9NZU7	Q9nz17 homo sapien
7	1085	33.0	550	11	Q9J3Z5	Q9j3z5 mus musculus
8	1066.5	32.4	558	4	Q9UYK6	Q9uik6 homo sapien
9	895	27.2	474	4	Q8WYG3	Q8wyg3 homo sapien
10	405.5	12.3	2809	4	Q96JP8	Q96jp8 homo sapien
11	402	12.2	1174	11	Q9K5H8	Q9k5h8 mus musculus
12	400.5	12.2	3857	11	Q88840	Q88840 mus musculus
13	396	12.0	2906	11	Q9WUJ9	Q9wu9 rattus norv
14	395.5	12.0	2872	11	Q9WUH8	Q9wuh8 rattus norv
15	385.5	11.7	608	11	Q9DBE2	Q9dbe2 mus musculus
16	384	11.7	708	13	P87363	P87363 gallus gall

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Query Match      88.5%; Score 2911; DB 11; Length 578;
Best local Similarity 88.1%; Pred. No. 5,2e-226;
Matches 510; Conservative 31; Mismatches 36; Indels 2; Gaps 2;

QY 1 MDELLALVLSYLLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPFY 60
DB 1 MAVLLAAVLASSLYLQVAADFGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPFY 60
QY 61 VLKRIARICOLKAVCOIPKCKHCEICGNPKCKHCHGYACKTCIOVLNKGKLPKPCXKR 120
DB 61 VLKRIARICOLKAVCOIPKCKHCEICGNPKCKHCHGYACKTCIOVLNKGKLPKPCXKR 120
QY 121 CMNTYGYKCYCLNGYMLMDGSCSSALTCGMANCOYGDVWVGQIRCOQSPSPGLQAPD 180
DB 121 CMNTYGYKCYCLNGYMLMDGSCSSALTCGMANCOYGDVWVGQIRCOQSPSPGLQAPD 180
QY 181 GRTCDVDECATGRVSCPRFQCVNTFGSYICKCKHGFGLMYIGGYQCHIDECSLGQY 240
DB 181 GRTCDVDECATGRVSCPRFQCVNTFGSYICKCKHGFGLMYIGGYQCHIDECSLGQY 240
QY 241 QCSSFANCYNVRSYKCKCKEGYQGGTCTVYIPKVMIEPSGPVHVPKGNCTILKGYTON 300
DB 241 QCSSFANCYNVRSYKCKCKEGYQGGTCTVYIPKVMIEPSGPVHVPKGNCTILKGYTON 300
QY 301 NNWIPDVGSTWMPKTPYIPPIITNRPSTKPTTRTPKPTPIPTPPPPPLPTTELRL-TPL 359
DB 301 NNWIPDVGSTWMPKTPYIPPIITNRPSTKPTTRTPKPTPIPTPPPPPLPTTELRL-TPL 359
QY 360 PPTTPTTGLTTIAPAASPTPGGIVDNRVQDQKPRGVDVFPKPSNDLFEIFEIE 419
DB 360 PPTTPTTGLTTIAPAASPTPGGIVDNRVQDQKPRGVDVFPKPSNDLFEIFEIE 419
QY 420 RGVSADEEVDDPGLIHSNCFDGLCGWIREKDSLDHETARDPAGGYLTVSAKAPG 479
DB 420 RGVSADEEVDDPGLIHSNCFDGLCGWIREKDSLDHETARDPAGGYLTVSAKAPG 479
QY 480 GKAARLVPLGRMLHSGDLCLSPKHKVTGLHSGTLQVFKHGAIGAALWGRNGHGWQ 539
DB 480 GKAARLVPLGRMLHSGDLCLSPKHKVTGLHSGTLQVFKHGAIGAALWGRNGHGWQ 539
QY 540 TQITLRGADIKSVFKCKEKRGRHTGEIGLDDVSLKRGHC 578
DB 540 TQITLRGADIKSVFKCKEKRGRHTGEIGLDDVSLKRGHC 578

RESULT 2
Q923T5 PRELIMINARY; PRT; 609 AA.
ID Q923T5
AC Q923T5;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE Nephronectin.
GN NPNT OR NEPH1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCHI_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Brandenberger R., Schmidt A., Linton J., Hackus C., Wang D., Denda S.,
KA Muller U., Reichardt I.F.;
RT Identification and Characterization of Nephronectin, a Novel ECM
RT Protein that is Associated with Integrin alpha8beta1 in the Embryonic
RT Kidney.*;
RL J. Cell Biol. 0:0-0(2001).
CC -!- SIMILARITY: CONTAINS 1 MAM DOMAIN.
DR EMHL; AF197008; AAK84392.1;
DR MGD; MG1:2148811; Npnt.
DR InterPro: IPR000152; Asx-hydroxyl.
DR InterPro: IPR000561; EGF-like.

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DR InterPro: IPR001861; EGF_Ca.
DR InterPro: IPR000998; MAM_domain.
DR Pfam: PF00008; EGF_4.
DR Pfam: PF00629; MAM_1.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_3.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; UNKNOWN_4.
DR PROSITE: PS01187; EGF_CA; UNKNOWN_3.
DR PROSITE: PS00060; MAM_2; 1.
KW Glycoprotein.
SQ SEQUENCE 609 AA; 67061 MW; 44C45DE4BHEC4HMC CR764;

Query Match      87.7%; Score 2885.5; DB 11; Length 609;
Best local Similarity 83.6%; Pred. No. 6,3e-224;
Matches 510; Conservative 31; Mismatches 46; Indels 44; Gaps 4;

QY 1 MDELLALVLSYLLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPFY 60
DB 1 MAVLLAAVLASSLYLQVAADFGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPFY 60
QY 61 VLKRIARICOLKAVCOIPKCKHCEICGNPKCKHCHGYACKTCIOVLNKGKLPKPCXKR 105
DB 61 VLKRIARICOLKAVCOIPKCKHCEICGNPKCKHCHGYACKTCIOVLNKGKLPKPCXKR 120
QY 106 -----VLNEGGLKPRCKHRCMNTYGYKCYCLNGYMLMDGSCSSALTC 149
DB 121 PGPDPHQAQTNVPSHDLNKGGLKIPKPKHRCMNTYGYKCYCLNGYMLMDGSCSSALTC 180
QY 150 CSMANCOYGDVWVGQIRCOQSPSPGLQAPDGRVDECATGRVSCPRFQCVNTFGS 209
DB 181 CSMANCOYGDVWVGQIRCOQSPSPGLQAPDGRVDECATGRVSCPRFQCVNTFGS 240
QY 210 YICKCKHGFGLMYIGGYQCHIDECSLGQYQCHIDECSLGQYQCHIDECSLGQY 269
DB 241 YICKCKHGFGLMYIGGYQCHIDECSLGQYQCHIDECSLGQYQCHIDECSLGQY 400
QY 270 CVYIPKVMIEPSGPVHVPKGNCTILKGYTONNNNIPDVGSTWMPKTPYIPPIITNRPST 429
DB 301 CVYIPKVMIEPSGPVHVPKGNCTILKGYTONNNNIPDVGSTWMPKTPYIPPIITNRPST 460
QY 330 KPTTPTTGLTTIAPAASPTPGGIVDNRVQDQKPRGVDVFPKPSNDLFEIFEIE 488
DB 361 KPTTPTTGLTTIAPAASPTPGGIVDNRVQDQKPRGVDVFPKPSNDLFEIFEIE 419
QY 389 NRVQDQKPRGVDVFPKPSNDLFEIFEIFEIFEIFEIFEIFEIFEIFEIFEIFEIFE 448
DB 420 NRVQDQKPRGVDVFPKPSNDLFEIFEIFEIFEIFEIFEIFEIFEIFEIFEIFEIFE 479
QY 449 IREKNDLHWPTRDPAGGYLTVSAKAPGKAAKLVLPGLHSGDLCLSPKHKVTG 508
DB 480 IREKNDLHWPTRDPAGGYLTVSAKAPGKAAKLVLPGLHSGDLCLSPKHKVTG 539
QY 509 LHSCTLQVFKHGAIGAALWGRNGHGWQITLRGADIKSVFKCKEKRGRHTGEIGL 568
DB 540 LHSCTLQVFKHGAIGAALWGRNGHGWQITLRGADIKSVFKCKEKRGRHTGEIGL 599
QY 569 DDVSLKRGHC 578
DB 600 DDVSLKRGHC 609

RESULT 3
Q91V88 PRELIMINARY; PRT; 561 AA.
ID Q91V88
AC Q91V88;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE POEM (NPHRONECTIN short isoform).
GN NPNT OR POEM OR NEPH1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6;
RX MEDLINE:21551216; PubMed:11546798;
RA Morimura N., Tezuka Y., Watanabe N., Yasuda M., Miyatani S.,
RA Hozumi N., Tezuka K.;
RT "Molecular cloning of POEM, A novel adhesion molecule that interacts
with alpha8beta1 integrin.";
RL J. Biol. Chem. 276:42172-42181(2001).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN-NIH SWISS; TISSUE=KIDNEY;
RX MEDLINE:21363579; PubMed:11470831;
RA Brandenberger R., Schmidt A., Linton J., Wang D., Backus C., Denda S.,
RA Muller U., Reichardt L.F.;
RT "Identification and characterization of a novel extracellular matrix
protein nephronectin that is associated with integrin alpha8beta1 in
the embryonic kidney.";
RL J. Cell Biol. 154:447-458(2001).
CC -!- SIMILARITY: CONTAINS 1 MAM DOMAIN.
DR EMBL: AB059656; BAB69692.1; -;
DR EMBL: AY035898; AAK96010.1; -;
DR MGD; MGI:2148811; Npnt.
DR InterPro: IPR000152; ASX_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR000998; MAM_domain.
DR Pfam: PF00008; EGF; 4.
DR Pfam: PF00629; MAM; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_3.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; UNKNOWN_3.
DR PROSITE: PS01187; EGF_CA; UNKNOWN_3.
DR PROSITE: PS00060; MAM_2; 1.
KW Glycoprotein.
SQ SEQUENCE 561 AA; 61490 MW; 697ACAA0EE3F506 CRC64;

Query Match 85.4%; Score 2809.5; DB 11; Length 561;
Best local Similarity 85.3%; Pred. No. 7.4e-218;
Matches 494; Conservative 30; Mismatches 36; Indels 19; Gaps 3;

QY 1 MDFLLALVLVSSLYLOAAAEFDGRWPQIVSSIGLCRYGRIDCCWGWAROSWGCQCPFY 60
Db 1 MAVLLAAVLASSLYLQVAADFGRWPQIVSSIGLCRYGRIDCCWGWAROSWGCQCP-- 58

QY 61 VLRQRIARICQLKAVCPQCKHCEGICPNKCKCHPCYAGKTCIQVLNECGLKPRCKHR 120
Db 59 -----VCQPCQKHGECVGNPKCKCHPCFAGKTCNQDLNECGLKPRCKHR 103

QY 121 CMNTYGYKCYCLNGYMLPDGSCSSALTCSMANCOYGCDDVWKGQIRCOCPSPGLQLAPD 180
Db 104 CMNTFGSYKCYCLNGYMLPDGSCSSALSCSMANCOYGCDDVWKGQVRCQCPSPGLQLAPD 163

QY 181 GRTCDVDECATGRASCPREOCVNTFGSYICKCHKGFDLMYIGGKYQCCHDIDECSLGQY 240
Db 164 GRTCDVDECATGRASCPREOCVNTFGSYICKCHKGFDLMYIGGKYQCCHDIDECSLGQH 223

QY 241 QCSSFARCYNVRGSKCKREGYOGDGLTCVYIPKVMIEPSGPIHPKNGTILKGDGTN 300
Db 224 QCSSYARCYNIHSGYKCKREGYEGDGLNCVYIPKVMIEPSGPIHPERNCTISKGDGH 283

QY 301 NNWIPDVGSTWPPKTYIPIITNRPVSKPTTRTPKPTPIPTPPPPPLPFLR-TPL 359
Db 284 ANRIPDAGSTRWPLKTYIPIITNRPVSKPTTRTPKPTPIPTPPPPPLPFLRPTPL 343

QY 360 PPTTPERTGLTTIAPAASTPPGGITVDNRVOTDPCKPRGDVFIPIPPSNDLFEIFEIE 419
Db 344 PP-TPERPSTRPTIATSTTTTAVITVDNRKIQTDPCKPRGDVFIPIPPINDLFEIFEIE 402

QY 420 RGVSAADFPAKDDPGLVHSCNFDHGLCGWI REKNDIHWEPTRDPAGQVLTVSAAKAPG 479
Db 403 RGVSADEEVKDDPGLIHSNCFDHLGCGWI REKNDISDLHWETARDPAGQVLTVSAAKAPG 462

QY 480 GKAAARLVLPGLRLMSSDCLCSFRHKVTGLHSGTLOVYFVRKKGAGUAGALWGRNGHGRQ 539
Db 463 GKAAARLVLRGLHLMHSGDCLCSFRHKVTGLHSGTLOVYFVRKKGAGUAGALWGRNGHGRQ 522

QY 540 TQITLRGADIKSVVPKGEKRRGHTGTEIGLDDVSLKKKGHC 578
Db 523 TQITLRGADVKSVPKGEKRRGHTGTEIGLDDVSLKKRGRC 561

RESULT 4
Q91XL5 PRELIMINARY; PRT: 592 AA.
AC Q91XL5;
DT 01-DEC-2001 (TREMHLrel. 19, Created)
DT 01-DEC-2001 (TREMHLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMHLrel. 21, Last annotation update)
DE Nephronectin.
GN NPNT OR NEPH1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-C57BL/6; TISSUE=KIDNEY;
RA Brandenberger R., Schmidt A., Linton J., Backus C., Wang D., Denda S.,
RA Muller U., Reichardt L.F.;
RT "Identification and Characterization of Nephronectin, a Novel ECM
Protein that is Associated with Integrin alpha8beta1 in the Embryonic
Kidney.";
RL J. Cell Biol. 0-0-0(2001).
CC -!- SIMILARITY: CONTAINS 1 MAM DOMAIN.
DR EMBL: AF397007; AAK84391.1; -;
DR MGD; MGI:2148811; Npnt.
DR InterPro: IPR000152; ASX_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR000998; MAM_domain.
DR Pfam: PF00008; EGF; 4.
DR Pfam: PF00629; MAM; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_3.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; UNKNOWN_3.
DR PROSITE: PS01187; EGF_CA; UNKNOWN_3.
DR PROSITE: PS00060; MAM_2; 1.
KW Glycoprotein.
SQ SEQUENCE 592 AA; 64944 MW; 21943B9077691396 CRC64;

Query Match 84.6%; Score 2784; DB 11; Length 592;
Best local Similarity 81.0%; Pred. No. 8.9e-216;
Matches 494; Conservative 30; Mismatches 36; Indels 50; Gaps 4;

QY 1 MDFLLALVLVSSLYLOAAAEFDGRWPQIVSSIGLCRYGRIDCCWGWAROSWGCQCPFY 60
Db 1 MAVLLAAVLASSLYLQVAADFGRWPQIVSSIGLCRYGRIDCCWGWAROSWGCQCP-- 58

QY 61 VLRQRIARICQLKAVCPQCKHCEGICPNKCKCHPCYAGKTCIQ----- 105
Db 59 -----VCQPCQKHGECVGNPKCKCHPCFAGKTCNQDESFIPTLDQSGEQ 103

QY 106 -----VLNECGLKPRCKHRMNTVGSYKCYCLNGYMLPDGSCSSALT 149
Db 104 PLPQPPDHOATNVPDRDLNECGLKPRCKHRMNTVGSYKCYCLNGYMLPDGSCSSALT 163

QY 150 CSMANCOYGCDDVWKGQIRCOCPSPGLQLAPDGRTCVDVDECATGRASCPREOCVNTFGS 209
Db 164 CSMANCOYGCDDVWKGQVRCQCPSPGLQLAPDGRTCVDVDECATGRVSCPRFOCVNTEGS 223

QY 210 YICKCHKGFDLMYIGGKYQCCHDIDECSLGQYQCSSFARCYNVRGSKCKCKEYQGDGLT 269
Db 224 YICKCHKGFDLMYIGGKYQCCHDIDECSLGQYQCSSYARCYNIHSGYKCKCRDGYEGDGLN 283

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QY 270 CVYIPKVMIRSGPIHVHKNGCTILKGTGTNNNWIIPDVGSTWMPKTPYIPPIITNPTS 329
DB 284 CVYIPKVMIRSGPIHVHKNGCTILKGTGTNNNWIIPDVGSTWMPKTPYIPPIITNPTS 343
QY 330 KPTTRPTPKPTPIPTPPPPPLPTELRL-TPLPPTTTPPTTGLTTIAPFAASTPPGGITVD 388
DB 344 KPTTRPTPKPTPIPTPPPPPLPTELRL-TPLPPTTTPPTTGLTTIAPFAASTPPGGITVD 402
QY 389 NRVTDPKPRGDPVPIPROPNDLFEIPIERGVSADDEKDDPGLVHSCNFDHGLCGW 448
DB 403 NRIQDPOKPRGDPVPIPROPNDLFEIPIERGVSADDEKDDPGLVHSCNFDHGLCGW 462
QY 449 IREKINDLHWEPIRIPAGCGVITVSAAKAPGCKAARLWLPGLMHSGLDGLSLFRKVTG 508
DB 463 IREKINDLHWEPIRIPAGCGVITVSAAKAPGCKAARLWLPGLMHSGLDGLSLFRKVTG 522
QY 509 LIISGTLQVFKKNGAALWCRNGSHGWRQTOITLRGADIKSVYFKGKRRGHTGETGL 568
DB 523 LIISGTLQVFKKNGAALWCRNGSHGWRQTOITLRGADIKSVYFKGKRRGHTGETGL 582
QY 569 DVSLKKGHC 578
DB 583 DVSLKKGRC 592

RESULT 5
QYNY67 PRELIMINARY: PRT: 554 AA.
AC Q9NY67;
BT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DI 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 61.4 kDa protein.
GN W80.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=TERATOCARCINOMA/NEURON;
RA Franco R.;
RI Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=TERATOCARCINOMA/NEURON;
RX MEDLINE-20241927; PubMed-10777661;
RA Buchner G., Orfanelli U., Quadri N., Bassi M.T., Andolfi G.;
RT "Identification of a new EGF-repeat-containing gene from human Xp22:
RT A candidate for developmental disorders.";
RL Genomics 65:16-23(2000).
CC -!- SIMILARITY: CONTAINS 1 MAM DOMAIN.
DB EMBL: AJ245671; CAB92132.1; -.
DR HSP; P00736; IAPQ.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF Ca.
DR InterPro: IPR000998; MAM_domain.
DR Pfam: PF00008; EGF; 4.
DR SMART: SM00179; EGF_CA; 3.
DR SMART: SM00001; EGF-like; 2.
DR SMART: SM00137; MAM; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 3.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 3.
DR PROSITE: PS00060; MAM_2; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation;
KW Hypothetical protein; Repeat.
SQ SEQUENCE 554 AA; 6136 MW; D519238F2A604101 CRC64;
Query Match 33.3%; Score 1096; DB 4; Length 554;

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Host Local Similarity 37.9%; Pred. No. 5, 7c-H0;
Matches 217; Conservative 99; Mismatches 168; Indels 88; Gaps 15;
QY 34 GLCYGRIDCCWAKQSGQCPFFVYLKQRIARICQLKAVQCQPKKIGETIGNKCK 94
DB 39 GVCHYCKIACCCYWRNRNKGVC-----ATCEGCKGKCGVGNKCK 81
QY 94 CHPGACKTCIQVINEGLKPRPKKRCMTYGSYKCYCLNGYMLMDFGSSALFESMA 154
DB 82 CFPGYTKTCSQVNEGCKMPKPCQHCRCVNTHSYKCFGLSGHLMFDPATCVNSRTCA 141
QY 154 NCQYGCIVWKGQIHCQCPSPHQLQIAPGRICVIVDECATCRASDPKRCQVNFPGSYCK 214
DB 142 NCQYSCDPEFGVPCICPSSGLRIAPNCRQCLDDDEACGKVICPYNRKCVNFGSYCK 201
QY 214 CHRGFDLMYIGGKQYQCHIDECSLGQYQCSFARCYVNRGYSYKCKEYWGIGELICVYI 274
DB 202 CHIGFELQYISGRYDCIDINPCTMDSHTCSHHANCFNTGSEKCKQGYKGNLRCSA 261
QY 274 PKVMIRSGPIHVHKNGCTILKGTGTNNNWIIPDVGSTWMPKTPYIPPIITNPTSPTT 334
DB 262 PENSVK-----EVLARPGTI-----KDRIKKLLAHKNSMKKKA 294
QY 334 R---PDKPPTPIPTPPPPPLPTELRLTPTTPTTPTTGLTTIAPFAASTHG 383
DB 295 KIKNVTPPTPTPTP-----KVNLIQFNVEE---IVSRGNSHCKKCKEER 348
QY 384 ---GITVDNRVQ-----TDPKPRGDVFIKPROPNDLFEIPIERGVSADDEKADDPG 448
DB 339 MKEGLEDKREKALKNDIEKSLRGVFFPKVNEAGDFGLIIVORKALTSKLEKADLN 508
QY 434 VLVHSCNFDHGLCGWIRKINDLHWEPI-RIPAGCGVITVSAAKAPGCKAARLWLPGL 492
DB 399 ISV-DCSFNHCIGCDWKQREDDEDFDNPADRONALGCFYMAVPALAGHKKDIIGKLLIFDL 457
QY 493 MHSGLDGLSLFRKVTGILHSGTLQVFKKNGAALWCRNGSHGWRQTOITLRGADIKSVYFKGKRRGHTGETGL 548
DB 458 QPQSNFCILFDYRIAGDKVGRVFRV---NSNNALWIKTTSDEKWKCKLQIYQGLDA 515
QY 549 IKSVMFKGKRRGHTGETGLDVSLLKKGHCSE 580
DB 516 TKSLTFARCKGKGTGELAVDGVLIIVSGICPP 547

RESULT 6
QYNYL7 PRELIMINARY: PRT: 553 AA.
AC Q9NYL7;
BT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DI 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Epidermal growth factor repeat containing protein.
GN EGF6.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20079166; PubMed-10610727;
RA Yeung G., Mulero J.J., Bernitsen R.P., Loeb D.B., Dimauro R.;
RA "Cloning of a novel epidermal growth factor repeat containing gene
RT EGF6; expressed in tumor and fetal tissues.";
RL Genomics 62:304-307(1999).
CC -!- SIMILARITY: CONTAINS 1 MAM DOMAIN.
DR EMBL: AF186084; AAF27812.1; -.
DR HSP; P00736; IAPQ.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF Ca.
DR InterPro: IPR000998; MAM_domain.
DR Pfam: PF00008; EGF; 4.

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DR Pfam: PF00629; MAM; 1.
DR SMART: SM00179; EGF_CA; 3.
DR SMART: SM00001; EGF_Like; 2.
DR SMART: SM00137; MAM; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 3.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 3.
DR PROSITE: PS00060; MAM_2; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
SQ SEQUENCE 553 AA: 61314 MW: 2FF55F167857DE50 CRC64;

Query Match 33.2%; Score 1092.5; DB 4; Length 553;
Best local Similarity 37.3%; Pred. No. 1.1e-79;
Matches 215; Conservative 96; Mismatches 173; Indels 87; Gaps 14;

QY 34 GLCRYGGRIDCCMGWQSGQCPFFVLRQRIARICQLKAVQCPCCKHGEICGPNKCK 93
DB 39 GVCHYGTKLACCYCHRRNSKVCCE-----ATCEPCKEFCGCVGNKCK 81

QY 94 CHFGYAGTKCIQVINEGCLKPRCKHRCMNTYGSYCYCLNGYMLMPDGCSSALTCMA 153
DB 82 CFPGYGTCTQSDVNECGMKPRPCQHRVNTHGSYKFCFLSGHMLLPDTCVNSRTCAMI 141

QY 154 NCQYGCDDVWVKQIRCOCPSPGLQAPDGRVCVDVDECATGRASCPRCQVNTFGSYCK 213
DB 142 NCQYSCDETEGPOCLCPSSGLRLAPNGRCLDIDECASGVICPYNRRCVNTFGSYCK 201

QY 214 CHKGFDMYIGGKYCHDIDCSLGQYQCSFARCVNVRGYSYCKKEGYGGLTCVYI 273
DB 202 CHIGFELQYISCRYDCIDINCTWDSHTCSHANCFTQSFCKCKQGYGNGLRCSAI 261

QY 274 PKVMEPSGPIHVPKGNGLTKGDTGNMNPDPVSTWPPKTPYIPPIITNRTSKPTT 333
DB 262 PENSVK-----EVLKAPGTI-----KDRKKLLAHKNSMKKA 294

QY 334 R---PTKPTPIPTPPPPPLPTLPTPTPTPTPTTGLTTIAPASIPPG----- 383
DB 295 KIKNVTPEPTPTPT-----KYNLPFNVEE-----IVSRGNSHGKKGNEEK 338

QY 384 ---GITVDNRVQ---TDPQKRGDVFIPROPNSDLFEIFEIERGVSADDEAKDDPGV 434
DB 339 MKGLEDHKKREKALKNDXERSLRGDVFPKVNAGEFGLLVORALKTSKLEHKDLNI 398

QY 435 LVHSCNFDHGLCGWIREKNDLHWEPI-RDPAGQYLTVSAAPGKAARLVLPGLRLM 493
DB 399 SV-DCSENHGICDWKQREDQFQWNPADRONAIGFYMAVPALAGHKDKDGLKLLPDLQ 457

QY 494 HSGDCLSFHVKVTLHSGTQLQVFRKHGAHGAALWGRNGHG--WRQTOITL-RGAD-I 549
DB 458 PQSNFCLLDYRLAGDKVGLRVFVK--NSNNALAEKTTSEDEKWKTKIQLYOGTDTAT 515

QY 550 KSVVFKGKRRGHTGEIGLDDVSLKKGHCSE 580
DB 516 KSLIFEARGKGTKEIAVDGVLLVSGLCPD 546

RESULT 7
Q9JJZ5 PRELIMINARY; PRT; 550 AA.
AC Q9JJZ5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 61.5 kDa protein.
GN EGF-L6 OR W80.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Franco R.;

Submitted (AUG-1999) to the EMBL/GenBank/UDRJ databases.
[12]
SEQUENCE FROM N.A.
MEDLINE=20241927; PubMed=10777661;
RA Buchner G., Orfanelli U., Quaderi M., Bassi M.T., Andolfi G.;
RT Identification of a new EGF-repeat-containing gene from human Xp22;
RT Candidates for developmental disorders.;
RL Genomics 65:16-23(2000).
CC -!- SIMILARITY: CONTAINS 1 MAM DOMAIN.
DR EMBL: AJ245672; CAB92138.1; --
DR BSSP: P35555; 1EMN.
DR MGD; MG1:1858599; Egf16.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF_Like.
DR InterPro: IPR001881; EGF_CA.
DR InterPro: IPR000998; MAM_domain.
DR Pfam: PF00008; EGF_4.
DR Pfam: PF00629; MAM_1.
DR SMART: SM00179; EGF_CA; 3.
DR SMART: SM00001; EGF_Like; 2.
DR SMART: SM00137; MAM; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 3.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 3.
DR PROSITE: PS00060; MAM_2; 1.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation;
KW Hypothetical protein; Repeat.
SQ SEQUENCE 550 AA: 61520 MW: DEF936325C9F31B3 CRC64;

Query Match 33.0%; Score 1085; DB 11; Length 550;
Best local Similarity 38.3%; Pred. No. 4.3e-79;
Matches 217; Conservative 93; Mismatches 180; Indels 76; Gaps 13;

QY 34 GLCRYGGRIDCCMGWQSGQCPFFVLRQRIARICQLKAVQCPCCKHGEICGPNKCK 93
DB 37 GVOYGTGMACCTGWRKNNKVCCE-----AMCEPKCKEFCGCVGNKCK 79

QY 94 CHFGYAGTKCIQVINEGCLKPRCKHRCMNTYGSYCYCLNGYMLMPDGCSSALTCMA 153
DB 80 CFPGYGTCTQSDVNECGVKPRPCQHRVNTHGSYKFCFLSGHMLLPDTCVNSRTCARL 139

QY 154 NCQYGCDDVWVKQIRCOCPSPGLQAPDGRVCVDVDECATGRASCPRCQVNTFGSYCK 213
DB 140 NCQYGCDETEGPRCVCPSGLRLAPNGRVCCLDIDECASKAVCPNRRCVNTFGSYCK 199

QY 214 CHKGFDMYIGGKYCHDIDCSLGQYQCSFARCVNVRGYSYCKKEGYGGLTCVYI 273
DB 200 CHIGFELKYIGRYDCVDINECALNTHPCSPHANCNLTGSPFKCKQGYGNGLQCSVI 259

QY 274 PKVMEPSGPIHVPKGNGLTKGDTGNMNPDPVSTWPPKTPYIPPIITNRTSKPTT 333
DB 260 PENSVK-----EILTAPGTI-----KDRKKLLAHKRTMKKKV 292

QY 334 R---PTKPTPIPTPPPPPLPTLPTPTPTPTPTTGLTTIAPASIPPG----- 380
DB 293 KLMVTPRPASTRVP-----KYNLPYSSEEGYSGRGNVDYDGEQKKEGKRERLEE 342

QY 381 PPGITVDNRVQDTPQKRGDVFIPROPNSDLFEIFEIERGVSADDEAKDDPGVLIHSCN 440
DB 343 EKGEKTLNRFVQER-RTLRGDVFSPKVNAEADLDLVYQKRELNSKLKHKDLNLSV-DCS 400

QY 441 FDHGLCGWIREKNDLHWEPI-RDPAGQYLTVSAAPGKAARLVLPGLRLMHISGDLG 499
DB 401 FDLGVCDDKQDREDDFDWHPADRDNDVGYMVPALAGHKKNIGRLKLLPLNLTQSNFC 460

QY 500 LSPRHKVTGLHSGTQLQVFRKHGAHGAALW--GRNGHGWRQTOITL-RGAD-IKSVFVK 555
DB 461 LLEDYRLAGDKVGLRVFVK--NSNNALAEKTTSEDEKWKTKIQLYOGTIDTKSVIFE 518

QY 556 GEKERGHTGEIGLDDVSLKKGHCSE 581
DB 519 AERKGTGTGTAVDGVLLVSGLCPPD 544

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RESULT 8
Q90FK6 PRELIMINARY: PRT: 558 AA.
AC Q90FK6:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2002 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 61.8 kDa protein (Fragment).
GN DKE2P564P2063.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Dusterthoof A., Lauber J., Mowes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 MAM DOMAIN.
DR EMBL: AL117610; CAB56014.1; -.
DR BSSP: P00736; IAPQ.
DR InterPro: IPR000152; ASX_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR000998; MAM_domain.
DR Pfam: PF00008; EGF_4.
DR Pfam: PF00629; MAM_1.
DR SMART: SM00179; EGF_CA; 3.
DR SMART: SM00001; EGF_Like; 2.
DR SMART: SM00137; MAM; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 2.
DR PROSITE: PS00060; MAM_2; 1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation;
KW Hypothetical protein; Repeat.
FT NON_TER 1
SQ SEQUENCE 558 AA; 61828 MW; AA38D7DCE402BFA3 CRC64;

Query Match 32.4%; Score 1066.5; DB 4; Length 558;
Best local Similarity 37.5%; Pred. No. 1.4e-77;
Matches 214; Conservative 95; Mismatches 175; Indels 87; Gaps 15;

QY 34 GLCRYGGRIDCCGWAROSWGCOCFFYVLRQRIARICQLAAVCOPCKHGECIGPNCK 93
DB 44 GVCHGTKLACCYGWRNSKVCE-----ATCPGCKPGRGVPNCKR 86

QY 94 CHPGYAGKTCIQVLENGELKPRCKHRCMNTYGSYKCYCLNGYMLPDPGSGSALLTCSMA 153
DB 87 CLPGYTGKTCSDVNECGMKPRPCQHRVNTINGSYKCFCLSGHMLMPDATCVYSRTCAI 146

QY 154 NCQYGCDDVVKQI/RCOCHSPGLQIAPDGRCTVDVDECATGRASCPRFKOCVNTFGSYCK 213
DB 147 NCQYSCDETDEGPQCLPSSGLRLAPNGRGLDIDECASGRVICPYNRCVNTFGSYCK 206

QY 214 CHKGFDLMYIGKCYOCHDIDECISLQYOCSSSFARCYNVRGSKCKEGYCGDGLTCVYI 273
DB 207 CHIGFELQYISGRYDCIDINCTMISHYSSSHANCFTNGSKCKCKGKNGKRCSAI 266

QY 274 PKVMIEPSGPIHVPGKNGTILKGDGTGNNNWIPDVGSTWMPKTPYIPPIITNRPSTKPTT 333
DB 267 PENSVK-----EVLRAPTI-----KDIRKLLAIKNSMKKKA 299

QY 334 R---PTPKPTPIPTPPPPPLTELRTPLPTTPTPTTGLTTTAPAASTPPG----- 383
DB 300 KIKNVIPEPTPTPT-----KVLQPFNVE---GI---VSRGNSHGKKGNEEK 343

QY 384 ---GITVDNRVQ-----TDQPKPRGDVFIPRQPSNDLFEIFEIERGSVADDEAKDPGV 434
DB 344 MKEGLEDKREKKA/KNIDIEHRSRGDVFPPKVNFAFEGILIVORKALT/SKLEHKDLNI 403

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QY 435 LVHSONFDHGLCGWIRKDNBLHWPPI-RDPAQGVLTVAAKAKGCKAAKRLVLPAGKRL 494
DB 404 SV-DCSENHGICDKWQDREDFDNPALRONAIGFYMAVPALAGIKKIKLGLLPLQL 462

QY 494 HSGDILCLSFRRHKVTGLHSGTLOVVRKHGAHGAALWGNNGHG--WRGTUTTLRGAD 1549
DB 463 POSNFCSLFDYRIAGDKVKGLRVFVK--NSNNALAWKKTTSDEKWKTKGKLYQYQTHAT 520

QY 550 KSVVPKREKRGHTGEIGLDVSLKKGHCSE 580
DB 521 KSTIPFAHKGKGTGCTAVDCVILVSGICM 551

RESULT 9
Q8WYG3 PRELIMINARY: PRT: 474 AA.
AC Q8WYG3:
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 53.1 kDa protein.
GN P648.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Gu J.X., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
RA Yu J., Han L.H.;
RT "Novel human cDNA clones with function of inhibiting cancer cell
RT growth.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF193055; AAG2483.1; -.
DR InterPro: IPR000152; ASX_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR000998; MAM_domain.
DR Pfam: PF00008; EGF_4.
DR Pfam: PF00629; MAM_1.
DR SMART: SM00181; EGF_4.
DR SMART: SM00179; EGF_CA; 4.
DR SMART: SM00137; MAM; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_3.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
DR PROSITE: PS01187; EGF_CA; UNKNOWN_3.
DR PROSITE: PS00060; MAM_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 474 AA; 53144 MW; 5F116F0DF91AC8BD CRC64;

Query Match 27.2%; Score 895; DB 4; Length 474;
Best local Similarity 36.5%; Pred. No. 7e-64;
Matches 184; Conservative 89; Mismatches 161; Indels 70; Gaps 13;

QY 101 KTCQVLENGELKPRCKHRCMNTYGSYKCYCLNGYMLPDPGSGSALLTCSMANFGVGT 160
DB 10 ETCSDVNECGMKPRPCQHRVNTINGSYKCFCLSGHMLMPDATCVNSHTAMINQYSCE 69

QY 161 VVKQI/RCOCHSPGLQIAPDGRCTVDVDECATGRASCPRFKOCVNTFGSYCK/RKGFGL 220
DB 70 DTEGPQCLPSSGLRLAPNGRGLDIDECASGRVICPYNRCVNTFGSYCK/RHGFEL 129

QY 221 MYIGKCYOCHDIDECISLQYOCSSSFARCYNVRGSKCKEGYCGDGLTCVYIPKVMIEP 280
DB 130 QYISGRYDCIDINCTMISHYSSSHANCFTNGSKCKCKGKNGKRC/SAIPENSVK 188

QY 281 SGPIHVPGKNGTILKGDGTGNNNWIPDVGSTWMPKTPYIPPIITNRPSTKPTT--- 437
DB 189 ----EVLRAPTI-----KDIRKLLAIKNSMKKKA/KKNVTP 222

QY 338 KPTPIPTPPPPPPPLTELRTPLPTTPTPTTGLTTTAPAASTPPG----- 487

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Db 223 EPTPTPT-----KVNLPFNTEE-----IVSRGNSHGKKGNEKKMGLEGLD 266
Qy 388 DNRVQ-----TDPKRGDVFIPROPSNDLFEIFEIRGYSADDEAKDDPGVLVHSCNF 441
Db 267 EKREKALKNDIEKSLRGDVFPEKNEACRFGILLVORKALTSKLEKHLNLSV-DCSF 325
Qy 442 DHGLCCWIREKNDLHWEP1-RDPAGQYLTVSAKAPGCKAARLVLPICRI.MHSGDLCL 500
Db 326 NHGICDMQDREDDFMNPDADNAIGFYMAVPALAGHKDIDIGRLKLLPDLQPSNFC 385
Qy 501 SFRHKVTCIHSCTIQVFVKRKHCAALWGRNGCHG--WROTOITL-RGAD-IKSVVFKG 556
Db 386 LFDYKLAGDKVGLRVFKV--NSNLAWEKTTSEDEKWKTKIQLYQGTDATAIIFEA 443
Qy 557 EKRRHGTGEIGLDVSLKKHCHSE 580
Db 444 ERGKGTGEIAVDGVLIVSGLCPLD 467

RESULT 10
Q96JP8 PRELIMINARY; PRT; 2809 AA.
AC Q96JP8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Fibrillin3.
GN KIAA1776.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=21245130; PubMed=11347906;
RA Nagase T., Nakayama M., Nakajima D., Kikuno R., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XX.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 8:85-95(2001).
DR EMBL; AB053450; BAB47408.1; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR002212; Fibril-assoc.
DR Pfam; PF00008; EGF; 45.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_41.
DR PROSITE; PS00022; EGF_1; UNKNOWN_2.
DR PROSITE; PS01186; EGF_2; UNKNOWN_36.
DR PROSITE; PS01187; EGF_CA; UNKNOWN_40.
SQ SEQUENCE 2809 AA; 300323 MW; 20C04CC006C0161F CRC64;

Query Match 12.38; Score 405.5; DR 4; Length 2809;
Best Local Similarity 36.68; Pred. No. 1.5e-23;
Matches 94; Conservative 26; Mismatches 98; Indels 39; Gaps 13;

Qy 35 LCRVG-----GRIDCCMGARQSGOCQPPYVLKRIARI-----RCQLKAVCQPRCKHG 84
Db 1081 LCRGTCNTNGSYKC-----OCPPCHEITAKGTACEDIDECSLS----DGICPHG 1127
Qy 85 EC---IGNKCKCHPGYAG---RTCIQVLNCEGLKPRCKHRCMNTYGSYKCYCLANGYM 137
Db 1128 OCNVNIGAFQCSCHAGFSTPDRCQCVDI-NFCRVNGCGDVHCINTGYSYKSCGGQYS 1186
Qy 138 LMPDG-SCSSAITC---SMANCOYG-CDVVKQCIRCCQSPGLQIAPDGRTCVDVDECATG 193
Db 1187 LMPDGRACADVDECEENPRVCDQGHCTNMPGGHRCLC-YDGFMATPD MRTCTVDVDECDLN 1245
Qy 194 NASCPRFPROCVNTFGSYICKCHKFDLMYIGKYOCHDIDFCSLGOYCCSFARCYNVRG 253
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Db 1246 PHIC-LHGDCHNTKGSFVCHCQLQY--MVRKGAIGCSVDVDECHVGGHNCUSHASCLNIPC 1302
Qy 254 SYKCKKEGYGGDLTIC 270
Db 1303 SFSCRLPLPGWVGDFEC 1319

RESULT 11
Q99K58 PRELIMINARY; PRT; 1174 AA.
AC Q99K58;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to fibulin 2.
GN FBLN2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005443; AAH05443.1; -.
DR HSP; P00736; IAPQ.
DR MGD; MGI:95488; Fbln2.
DR InterPro; IPR000020; Anaphylatoxin.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_CA.
DR Pfam; PF01821; ANATO; 2.
DR Pfam; PF00008; EGF; 6.
DR SMART; SM00104; ANATO; 3.
DR SMART; SM00181; EGF; 11.
DR SMART; SM00179; EGF_CA; 9.
DR PROSITE; PS01177; ANAPHYLATOXIN_1; 3.
DR PROSITE; PS01178; ANAPHYLATOXIN_2; 3.
DR PROSITE; PS00010; ASX_HYDROXYL; 5.
DR PROSITE; PS01186; EGF_2; 5.
DR PROSITE; PS01187; EGF_CA; 9.
KW Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
SQ SEQUENCE 1174 AA; 126460 MW; 8D62BAC710FBA688 CRC64;

Query Match 12.28; Score 402; DB 11; Length 1174;
Best Local Similarity 38.98; Pred. No. 9.9e-24;
Matches 88; Conservative 27; Mismatches 86; Indels 25; Gaps 12;

Qy 80 RCKHCE-CI---GPNKCKCHPGYA----GKTCIQVLNFCGLKLP-RPCKHRCMNTYGSYKC 130
Db 858 RCGEGLCYNLPGSYRCDCPKPGFQDFAFGRTCIDV-NECWVSGRLCQHTCENTPGSYRC 916
Qy 131 YCLNGYMLPDGS-CSSALTCSMANCOYGDVVKQIRCCQSPGLQIAPDGRTCVDVDE 189
Db 917 SCAAGPILADGKHCEVDNCETRRCQECANIVGTCQVC-ROGYQIADGHTCTDIDE 975
Qy 190 CATGRASCPROCVNTFGSYICK-KHGFELMYIGKYQCHDIDECSLGYQCSFARC 248
Db 976 CAQAGILCTFR-CVNVPGSYQACPEQGYTMANG--RSCKDLDECALGTHNCSAEATC 1032
Qy 249 YNVRCYSYK---CKKEGY-----QGDLCTCVIIPKVMIEPSGPIH 285
Db 1033 HNIQGSFRLCFDPPNVRVSVSETKCRITTCQDITECQTSPARITH 1078

RESULT 12
O88840 PRELIMINARY; PRT; 3857 AA.
AC O88840;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Mutant fibrillin-1.
```

GN FBNI.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID-10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-B10.D2;
RX MEDLINE-98069008; PubMed-9405944;
RA Hana C.A., Murai C., Casares S., Kasturi K., Nishimura H., Honjo T.,
RA Matsuda F.;
RT "Structure of the mutant fibrillin-1 gene in the tight skin (TSK)
RI mouse.";
RL DNA Res. 4:267-271(1997).
DR EMBL: AF007248; AAC62317.1;
DR HSSP: P35555; IADJ.
DR MGI: MGI:95489; Fbni.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR002557; Chitin_bind_Pera.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF-Ca.
DR InterPro: IPR002212; Fibril-assoc.
DR InterPro: IPR000822; Znf_C2H2.
DR Pfam: PF00008; EGF; 64.
DR PRINTS: PR00083; TB; 12.
DR SMART: SM00494; ChIBD2; 2.
DR SMART: SM00179; EGF_CA; 60.
DR SMART: SM00001; EGF-like; 4.
DR PROSITE: PS00010; ASX_HYDROXYL; 61.
DR PROSITE: PS00022; EGF_1; UNKNOWN_2.
DR PROSITE: PS01186; EGF_2; 50.
DR PROSITE: PS01187; EGF_CA; 61.
DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
SQ SEQUENCE 3857 AA; 418301 MW; 5BC0618BC527E04C CRC64;

Query Match 12.2%; Score 400.5; DB 11; Length 3857;
Best Local Similarity 31.7%; Pred. No. 5.4e-23;
Matches 104; Conservative 33; Mismatches 104; Indels 87; Gaps 15;

QY 35 LCRVY-----GRIDCCGWAHSGOCQPPVILKRIARI-----RCOLKAVCPKCRKHG 84
DB 1125 LCRGICINTEGSRG-----ECPGHQLSPNISACIDINECELSA---NLCPHG 1171
QY 85 EC---IGPNKCKCHPGYAGK-----TCTQVLNPGGLKPRCKHRCMNTYGSYKCYCINQYM 137
DB 1172 RCVNI.LGRYOCACNPGYHP.TDRI.LPCVDI-DKCSIMNGGCTFTCTNSDPSYKSCQPCFA 1230
QY 138 LMPD-GSCSSALTC--SMANQYQ-CDVVKGQIRCCQSPGLQAPDQRTCDV-----187
DB 1231 LMPDQSCDTDIDKCHDPIFNICDGGQCTNIPGFRIC-VDGFMASEDMKTCVDVNFCDLN 1289
QY 188 -----DKCATGRASCPFRFCVNTFGSYI 211
DB 1290 PNICLSGTGTCNTKGSFICIKDMYSGKKGKTKGTCTDINECEIGAINCGRIHVCNTNTAGSEK 1349
QY 212 CKCHKGFDIMYIGKYOCHDIDECISLGQYQCSFAPCYNVKSGYKCKEGYQCGDLTCV 271
DB 1350 CSCSPG---WICDGIKCTDIDECNSGTHMCSQAHCKNTKNSYKICLCKDGYTGIGFTCT 1405
QY 272 YIPKVMIEPSGPIHPVKGNGTILKGDG 299
DB 1406 DLD-----ECSENI.NI-CGNGQCI.NAPG 1428

RESULT 13
Q9WUH9
ID Q9WUH9 PRELIMINARY; PRT: 2906 AA.
AC Q9WUH9;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Fibrillin-2.

OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID-10116;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE-99350241; PubMed-10419698;
RX Yang Q., Ota K., Tian Y., Kumar A., Wada J., Kashihara N., Wallner E.,
RA Kanwar Y.S.;
RT "Cloning of rat fibrillin-2 cDNA and its role in branching
RI morphogenesis of embryonic lung.";
RL Dev. Biol. 212:229-242(1999).
DR EMBL: AF15060; AAD34439.1;
DR HSSP: P35555; IEMN.
DR InterPro: IPR002086; Aldehyde dehydr.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF-Ca.
DR InterPro: IPR001438; EGF-II.
DR InterPro: IPR002212; Fibril-assoc.
DR Pfam: PF00008; EGF; 46.
DR Pfam: PF00683; TB; 9.
DR PRINTS: PR00010; EGFHLOOD.
DR SMART: SM00179; EGF_CA; 42.
DR SMART: SM00001; EGF-like; 4.
DR PROSITE: PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
DR PROSITE: PS00010; ASX_HYDROXYL; 43.
DR PROSITE: PS00022; EGF_1; UNKNOWN_2.
DR PROSITE: PS01186; EGF_2; 36.
DR PROSITE: PS01187; EGF_CA; 43.
DR Calcium-binding; EGF-like domain; Glycoprotein; Hydroxylation; Repeat.
SQ SEQUENCE 2906 AA; 313371 MW; 9EF64E727044EF58 CRC64;

Query Match 12.0%; Score 396; DB 11; Length 2906;
Best Local Similarity 39.1%; Pred. No. 8.9e-24;
Matches 79; Conservative 33; Mismatches 74; Indels 16; Gaps 9;

QY 81 CKHGEK---IGPNKCKCHPGYAGK-----KTCTQVLNPGGLKPRCKHRCMNTYGSYKCYC 133
DB 1203 CRNCKCVNMICTYQCSNPGYQATPDHQCSDI-DKCMIMNGGCTFTCTNSDPSYKSCS 1261
QY 134 NGYMLMPDG-SCSSALTC--SMANQYQ-CDVVKGQIRCCQSPGLQAPDQRTCDV 189
DB 1262 EGYALMPDGRSCADIDECENNPDCDGGQCTNIPGFRICL-VIRGFMASDMKTCVDVNE 1420
QY 190 CATGRASCPFRFCVNTFGSYICKCHKGFDIMYIGKYOCHDIDECISLGQYQCSFAPCY 249
DB 1321 CDLPNITC-MEGECENTKGSFICIKDGYCGLQYVYK--KGATGCTDIDVDEIGAINLUMIASCL 1377
QY 250 NVKSGYKCKEGYQCGDLTCV 271
DB 1378 NVPGSFKSCHEGHWGNGIKCI 1399

RESULT 14
Q9WUH8
ID Q9WUH8 PRELIMINARY; PRT: 2872 AA.
AC Q9WUH8;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Fibrillin-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID-10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99032689; PubMed-9815129;
RA Kanwar Y.S., Ota K., Yang Q., Kumar A., Wada J., Kashihara N.,
RA Peterson D.R.;
RT "Isolation of rat fibrillin-1 cDNA and its relevance in metaphoric
RI development.";

RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King H., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzaroli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shihata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L., Wyshaw-Borls A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.
KI	*Functional annotation of a full-length mouse cDNA collection.*;
RL	Nature 409:685-690(2001).
DR	EMBL; AK005010; BAB23743.1; -
DR	HSP; P00743; ICCF.
DR	MGI; MG1:1919018; 1300015B04Rik.
DR	InterPro; IPK000152; ASX_hydroxyl.
DR	InterPro; IPK000561; EGF-like.
DR	InterPro; IPK001881; EGF_Ca.
DR	InterPro; IPK001007; VWF-C.
DR	Pfam; PF00008; EGF; 3.
DR	Pfam; PF00093; vwc; 3.
DR	SMART; SM00181; EGF; 5.
DR	SMART; SM00179; EGF_CA; 3.
DR	SMART; SM00214; VWC; 2.
DR	PROSITE; PS00010; ASX_HYDROXYL; 2.
DR	PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR	PROSITE; PS01186; EGF_2; 2.
DR	PROSITE; PS01187; EGF_CA; 3.
DR	PROSITE; PS01208; VWFC; UNKNOWN_2.
SO	SEQUENCE 608 AA; 6410 MW; 72P7136A82FF764F CRC64;

Query Match	11.7%; Score 385.5; DB 11; Length 608;
Best Local Similarity	26.5%; Pred. No. 9,5e+23;
Matches 122; Conservative 55; Mismatches 179; Indels 105; Gaps	

Oy	35	LCRYGGRIDCGWA-RQSGQCQPYYVLQRIRINQLKAVCPQCRKHGEICGNCKC 93	: : : : : : : : : : : :
Dd	44	VCLSGFGGCCPGWAPSMGSGHC-----TLPLCSFGCGSGICIAPNVGS 87	: : : : : : : : : : : :
Oy	94	CHPYAGKTCTIQVLNEGLKPRCKRMNTYGYKC----YCLNGYMLMPDG---SCS 145	: : : : : : : : : : : :
Dd	88	CQDEQGATCFEAGHSCG-----EYGCULTNHGGCOEVARVCVPGLMTETAVGIRCA 141	: : : : : : : : : : : :
Oy	146	SALTCSMANGCYGDVVKGIGRCQSPGLADGRTCVDDCATGRASCPFRFCQVN 205	: : : : : : : : : : : :
Dd	142	DIDRECLSSSCHGHCVNTEGGFVCEC-GPGMLSADRHSOOTDFC---LGTPCQORCN 196	: : : : : : : : : : : :
Oy	206	TFGSYICKCHKGFDLMYGKYOGHDIDEGSLGOYCSSHANCYNVKGSKCKRKPY-- 263	: : : : : : : : : : : :
Dd	197	SIGSYKSCRAGFILH--GNRHSCIDYNECRRPQERRVCHHTCHNVGVSFLCTCRPGFRL 254	: : : : : : : : : : : :
Oy	264	OGDLGTGVYLPKVMLEPSG--PIHVPKMGNTLLKGTIGNNNWIPIVGSITWWPPKPTYP 320	: : : : : : : : : : : :
Dd	255	RSDRVSEAFPAKLAPSAILQPRQHAKMSLIJL-----PRAG----- 292	: : : : : : : : : : : :
Oy	321	PIINRRTSKPTRPTPKPTPIPTPPPPPPLTELRLTLPPTTPE-----RPTTGLTTIA 375	: : : : : : : : : : : :
Dd	293	-----RALSPGHSP-----PGACPYPCVVRTISQPSITQVLPFTTFQTLISTPV 338	: : : : : : : : : : : :
Oy	376	PAASTPPGGITVDNRVQ---TDQPKRGIVFIIPQ-----SNILFEIFPHKGVSAADDE 427	: : : : : : : : : : : :
Dd	339	P-SSSPLCTLGPSSLQCAVGTFSSPRG----PESPKLAGSSSCWHL-----GATYESG 388	: : : : : : : : : : : :
Oy	428	AK-DDPGVLVHSCNFDHGLCCWIREKDNDIHWEPIRDPPAGE 467	: : : : : : : : : : : :
Dd	389	SRWNQPGCSQCIQQDGRVTGGVRCDATCSHPVPPRID--CG 427	: : : : : : : : : : : :

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Job time : 101 secs